

SEQUENCE LISTING

(1) General Information

- (i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.
- (ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel Activity and DNA sequence
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.
 - (B) STREET: 9 ? 19 Shimoshinjo 3-chome Higashiyodogawa-Ku
 - (C) CITY: Osaka
 - (D) STATE: Osaka
 - (E) COUNTRY: JAPAN
 - (F) ZIP: 533-0021
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage
 - (B) COMPUTER: IBM PS/2 or compatibles
 - (C) OPERATING SYSTEM: WINDOWS 95/97
 - (D) SOFTWARE: Microsoft Word 97
- (vi) CURRENT APPLICATION DATE:
 - (A) APPLICATION NUMBER: 09/381,810
 - (B) FILING DATE: 19-OCT-1999
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE
 - (A) APPLICATION NUMBER: JP09 094845
 - (B) FILING DATE: 28-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Burton A. Amernick
 - (B) REGISTRATION NUMBER: 24852
 - (C) REFERENCE/DOCKET NUMBER: 1581/00156
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)331-7111
 - (B) FAX: (202)293-6229

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH F342 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY F linear
- (ii) MORECULE TYPE F peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
      5              10              15
Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
      20              25              30
Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
      35              40              45
Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
      50              55              60
Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met
      65              70              75              80
Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala
      85              90              95
Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe

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[illegible]

GGCTCTGGAC	TGGGGACACA	GGGATAGCTG	AGCCCCAGCT	GGGGGTGGAA	GCTGAGCCAG	60
GGACAGTCAC	GGAGGAACAA	GATCAAGATG	CGCTGTAACT	GAGAAGCCCC	CAAGGCGGAG	120
GCTGAGAATC	AGAGACATTT	CAGCAGACAT	CTACAAATCT	GAAAGACAAA	AC ATG GTT	178
					Met Val	
					1	
CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC						226
Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser						
5			10		15	

TGG	TCC	GTG	ATA	GCA	AAG	ATC	CAG	GAA	ATA	CTG	CAG	AGG	AAG	ATG	GTG	274
Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg	Lys	Met	Val	
20						25					30					
CGA	GAG	TTC	CTG	GCC	GAG	TTC	ATG	AGC	ACA	TAT	GTC	ATG	ATG	GTA	TTC	322
Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val	Met	Met	Val	Phe	
35					40					45					50	
GGC	CTT	GGT	TCC	GTG	GCC	CAT	ATG	GTT	CTA	AAT	AAA	AAA	TAT	GGG	AGC	370
Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn	Lys	Lys	Tyr	Gly	Ser	
				55				60						65		
TAC	CTT	GGT	GTC	AAC	TTG	GGT	TTT	GGC	TTC	GGA	GTC	ACC	ATG	GGA	GTG	418
Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe	Gly	Val	Thr	Met	Gly	Val	
			70					75					80			
CAC	GTG	GCA	GGC	CGC	ATC	TCT	GGA	GCC	CAC	ATG	AAC	GCA	GCT	GTG	ACC	466
His	Val	Ala	Gly	Arg	Ile	Ser	Gly	Ala	His	Met	Asn	Ala	Ala	Val	Thr	
		85					90				95					
TTT	GCT	AAC	TGT	GCG	CTG	GGC	CGC	GTG	CCC	TGG	AGG	AAG	TTT	CCG	GTC	514
Phe	Ala	Asn	Cys	Ala	Leu	Gly	Arg	Val	Pro	Trp	Arg	Lys	Phe	Pro	Val	
100						105					110					
TAT	GTG	CTG	GGG	CAG	TTC	CTG	GGC	TCC	TTC	CTG	GCG	GCT	GCC	ACC	ATC	562
Tyr	Val	Leu	Gly	Gln	Phe	Leu	Gly	Ser	Phe	Leu	Ala	Ala	Ala	Thr	Ile	
115					120					125					130	
TAC	AGT	CTC	TTC	TAC	ACG	GCC	ATT	CTC	CAC	TTT	TCG	GGT	GGA	CAG	CTG	610
Tyr	Ser	Leu	Phe	Tyr	Thr	Ala	Ile	Leu	His	Phe	Ser	Gly	Gly	Gln	Leu	
				135					140					145		
ATG	GTG	ACC	GGT	CCC	GTC	GCT	ACA	GCT	GGC	ATT	TTT	GCC	ACC	TAC	CTT	658
Met	Val	Thr	Gly	Pro	Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr	Tyr	Leu	
			150					155					160			
CCT	GAT	CAC	ATG	ACA	TTG	TGG	CGG	GGC	TTC	CTG	AAT	GAG	GCG	TGG	CTG	706
Pro	Asp	His	Met	Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala	Trp	Leu	
		165					170					175				
ACC	GGG	ATG	CTC	CAG	CTG	TGT	CTC	TTC	GCC	ATC	ACG	GAC	CAG	GAG	AAC	754
Thr	Gly	Met	Leu	Gln	Leu	Cys	Leu	Phe	Ala	Thr	Thr	Asp	Gln	Glu	Asn	
	180					185				190						
AAC	CCA	GCA	CTG	CCA	GGA	ACA	GAG	GCG	CTG	GTG	ATA	GGC	ATC	CTC	GTG	802
Asn	Pro	Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Val	Ile	Gly	Ile	Leu	Val	
195					200					205					210	
GTC	ATC	ATC	GGG	GTG	TCC	CTT	GGC	ATG	AAC	ACA	GGA	TAT	GCC	ATC	AAC	850
Val	Ile	Ile	Gly	Val	Ser	Leu	Gly	Met	Asn	Thr	Gly	Tyr	Ala	Ile	Asn	
				215					220					225		
CCG	TCC	CGG	GAC	CTG	CCC	CCC	CGC	ATC	TTC	ACC	TTC	ATT	GCT	GGT	TGG	898
Pro	Ser	Arg	Asp	Leu	Pro	Pro	Arg	Ile	Phe	Thr	Phe	Ile	Ala	Gly	Trp	
			230					235					240			
GGC	AAA	CAG	GTC	TTC	AGC	AAT	GGG	GAG	AAC	TGG	TGG	TGG	GTG	CCA	GTG	946
Gly	Lys	Gln	Val	Phe	Ser	Asn	Gly	Glu	Asn	Trp	Trp	Trp	Val	Pro	Val	
		245					250					255				
GTG	GCA	CCA	CTT	CTG	GGT	GCC	TAT	CTA	GGT	GGC	ATC	ATC	TAC	CTG	GTC	994
Val	Ala	Pro	Leu	Leu	Gly	Ala	Tyr	Leu	Gly	Gly	Ile	Ile	Tyr	Leu	Val	
		260				265					270					
TTC	ATT	GGC	TCC	ACC	ATC	CCA	CGG	GAG	CCC	CTG	AAA	TTG	GAG	GAT	TCT	1042
Phe	Ile	Gly	Ser	Thr	Ile	Pro	Arg	Glu	Pro	Leu	Lys	Leu	Glu	Asp	Ser	
275					280					285					290	
GTG	GCG	TAT	GAA	GAC	CAC	GGG	ATA	ACC	GTA	TTG	CCC	AAG	ATG	GGA	TCT	1090
Val	Ala	Tyr	Glu	Asp	His	Gly	Ile	Thr	Val	Leu	Pro	Lys	Met	Gly	Ser	
				295					300					305		
CAT	GAA	CCC	ACG	ATC	TCT	CCC	CTC	ACC	CCC	GTC	TCT	GTG	AGC	CCT	GCC	1138
His	Glu	Pro	Thr	Ile	Ser	Pro	Leu	Thr	Pro	Val	Ser	Val	Ser	Pro	Ala	
			310					315						320		

